

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: Pasteur Merieux serums et vaccins  
(B) STREET: 58, avenue leclerc  
(C) CITY: Lyons  
(E) COUNTRY: France  
(F) POSTAL CODE: 69007

(A) NAME: Transgene  
(B) STREET: 11, rue de Molsheim  
(C) CITY: Strasbourg  
(E) COUNTRY: France  
(F) POSTAL CODE: 67000

(ii) TITLE OF INVENTION: Tbp2 fragments of N. meningitidis

(iii) NUMBER OF SEQUENCES: 35

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Tape  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
(EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: IM2169

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 60..119

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 120..2192

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 60..2192

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 120..1154

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1155..1748

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1749..2192

## (ix) FEATURE:

(A) NAME/KEY: misc\_binding  
(B) LOCATION: 127..1169

(x1) SEQUENCE DESCRIPTION : SEQ ID NO: 1:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT | 59  |
| ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT | 107 |
| Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe |     |
| -20 -15 -10 -5                                                  |     |
| TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT | 155 |
| Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser |     |
| 1 5 10                                                          |     |
| GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT | 203 |
| Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser |     |
| 15 20 25                                                        |     |
| TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG | 251 |
| Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala |     |
| 30 35 40                                                        |     |
| ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG | 299 |
| Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu |     |
| 45 50 55 60                                                     |     |
| GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA | 347 |
| Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys |     |
| 65 70 75                                                        |     |
| CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA | 395 |
| Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu |     |
| 80 85 90                                                        |     |
| ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA | 443 |
| Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser |     |
| 95 100 105                                                      |     |
| AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT | 491 |
| Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn |     |
| 110 115 120                                                     |     |
| CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT | 539 |
| Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe |     |
| 125 130 135 140                                                 |     |
| TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG | 587 |
| Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys |     |
| 145 150 155                                                     |     |
| TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA | 635 |
| Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg |     |
| 160 165 170                                                     |     |
| CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT | 683 |
| Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe |     |
| 175 180 185                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT<br>Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro<br>190 195 200     | 731  |
| TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC<br>Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser<br>205 210 215 220 | 779  |
| GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG<br>Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu<br>225 230 235     | 827  |
| GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA<br>Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys<br>240 245 250     | 875  |
| TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT<br>Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr<br>255 260 265     | 923  |
| AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA<br>Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile<br>270 275 280     | 971  |
| ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG<br>Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu<br>285 290 295 300 | 1019 |
| AAT GAA ACC AAA CTA CAT CCG TTT GTT TCC GAC TCG TCT TCT TTG AGC<br>Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser<br>305 310 315     | 1067 |
| GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG<br>Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu<br>320 325 330     | 1115 |
| AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC<br>Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp<br>335 340 345     | 1163 |
| AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA<br>Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala<br>350 355 360     | 1211 |
| TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG<br>Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr<br>365 370 375 380 | 1259 |
| GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT<br>Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn<br>385 390 395     | 1307 |
| CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG<br>Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met<br>400 405 410     | 1355 |
| ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT<br>Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp<br>415 420 425     | 1403 |
| AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG<br>Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr<br>430 435 440     | 1451 |

CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG 1499  
 Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly  
 445 450 455 460

GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA 1547  
 Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
 465 470 475

ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC 1595  
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
 480 485 490

GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA 1643  
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly  
 495 500 505

AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG 1691  
 Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
 510 515 520

TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA 1739  
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln  
 525 530 535 540

AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA 1787  
 Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr  
 545 550 555

AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA 1835  
 Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu  
 560 565 570

TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT 1883  
 Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala  
 575 580 585

GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC 1931  
 Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly  
 590 595 600

AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC 1979  
 Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu  
 605 610 615 620

GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC 2027  
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala  
 625 630 635

AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA 2075  
 Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly  
 640 645 650

TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA 2123  
 Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr  
 655 660 665

TCC AGC GAT GGA AAT TCA GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG 2171  
 Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala  
 670 675 680

AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA 2222  
 Lys Arg Gln Gln Pro Val Gln  
 685 690

GGCTTCAG

2230

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
 -20 -15 -10 -5  
 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
 1 5 10  
 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
 15 20 25  
 Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala  
 30 35 40  
 Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu  
 45 50 55 60  
 Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys  
 65 70 75  
 Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu  
 80 85 90  
 Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser  
 95 100 105  
 Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn  
 110 115 120  
 Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe  
 125 130 135 140  
 Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys  
 145 150 155  
 Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg  
 160 165 170  
 Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe  
 175 180 185  
 Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro  
 190 195 200  
 Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser  
 205 210 215 220  
 Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu  
 225 230 235

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys  
240 245 250  
Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr  
255 260 265  
Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile  
270 275 280  
Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu  
285 290 295 300  
Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser  
305 310 315  
Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu  
320 325 330  
Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp  
335 340 345  
Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala  
350 355 360  
Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr  
365 370 375 380  
Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn  
385 390 395  
Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met  
400 405 410  
Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp  
415 420 425  
Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr  
430 435 440  
Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly  
445 450 455 460  
Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
465 470 475  
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
480 485 490  
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly  
495 500 505  
Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
510 515 520  
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln  
525 530 535 540  
Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr  
545 550 555  
Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu  
560 565 570

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala  
 575 580 585  
 Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly  
 590 595 600  
 Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu  
 605 610 615 620  
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala  
 625 630 635  
 Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly  
 640 645 650  
 Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr  
 655 660 665  
 Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala  
 670 675 680  
 Lys Arg Gln Gln Pro Val Gln  
 685 690

(2) INFORMATION FOR SEQ ID NO. 3:

- 5
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1808 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: N. meningitidis  
 (B) STRAIN: IM2394
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..60
- 15 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 61..1797
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1797
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 61..1035
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1036..1386
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1387..1797
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_binding  
 (B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 3:

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT<br>Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe<br>-20 -15 -10 -5  | 48  |
| TTG TTG AGT GCT TGT CTG GGT GGC GGC GGC AGT TTC GAT TTG GAC AGC<br>Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser<br>1 5 10          | 96  |
| GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA<br>Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu<br>15 20 25        | 144 |
| AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG<br>Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala<br>30 35 40        | 192 |
| GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT<br>Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn<br>45 50 55 60     | 240 |
| CCT AAA TAT AAG GAA AAG CAC AAA CCA TTG GGT TCA ATG GAT TCG AAA<br>Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys<br>65 70 75        | 288 |
| AAA CTG CAA AGA GGA GAA CCA AAT AGT TTT AGT GAG AGG GAT GAA TTG<br>Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu<br>80 85 90        | 336 |
| GAA AAA AAA CGG GGT AGT TCT GAA CTT ATT GAA TCA AAA TGG GAA GAT<br>Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp<br>95 100 105      | 384 |
| GGG CAA AGT CGT GTA GTT GGT TAT ACA AAT TTC ACT TAT GTC CGT TCG<br>Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser<br>110 115 120     | 432 |
| GGA TAT GTT TAC CTT AAT AAA AAT AAT ATT GAT ATT AAG AAT AAT ATA<br>Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile<br>125 130 135 140 | 480 |
| GTT CTT TTT GGA CCT GAC GGA TAT CTT TAC TAT AAA GGG AAA GAA CCT<br>Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro<br>145 150 155     | 528 |
| TCC AAG GAG CTG CCA TCG GAA AAG ATA ACT TAT AAA GGT ACT TGG GAT<br>Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp<br>160 165 170     | 576 |
| TAT GTT ACT GAT GCT ATG GAA AAA CAA AGG TTT GAA GGA TTG GGT AGT<br>Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser<br>175 180 185     | 624 |
| GCA GCA GGA GGA GAT AAA TCG GGG GCG TTG TCT GCA TTA GAA GAA GGG<br>Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly<br>190 195 200     | 672 |
| GTA TTG CGT AAT CAG GCA GAG GCA TCA TCC GGT CAT ACC GAT TTT GGT<br>Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly<br>205 210 215 220 | 720 |



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATG ACT AGT GAG TTT GAG GTT GAT TTT TCT GAT AAA ACA ATA AAG GGC<br>Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly<br>225 230 235     | 768  |
| ACA CTT TAT CGT AAC AAC CGT ATT ACT CAA AAT AAT AGT GAA AAC AAA<br>Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys<br>240 245 250     | 816  |
| CAA ATA AAA ACT ACG CGT TAC ACC ATT CAA GCA ACT CTT CAC GGC AAC<br>Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn<br>255 260 265     | 864  |
| CGT TTC AAA GGT AAG GCG TTG GCG GCA GAT AAA GGT GCA ACA AAT GGA<br>Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly<br>270 275 280     | 912  |
| AGT CAT CCC TTT ATT TCC GAC TCC GAC AGT TTG GAA GGC GGA TTT TAC<br>Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr<br>285 290 295 300 | 960  |
| GGG CCG AAA GGC GAG GAA CTT GCC GGT AAA TTC TTG AGC AAC GAC AAC<br>Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn<br>305 310 315     | 1008 |
| AAA GTT GCA GCG GTG TTT GGT GCG AAG CAG AAA GAT AAG AAG GAT GGG<br>Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly<br>320 325 330     | 1056 |
| GAA AAC GCG GCA GGG CCT GCA AAG GAA ACC GTG ATA GAT GCA TAC CGT<br>Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg<br>335 340 345     | 1104 |
| ATT ACC GGC GAG GAG TTT AAG AAA GAG CAA ATA GAC AGT TTT GGA GAT<br>Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp<br>350 355 360     | 1152 |
| GTG AAA AAG CTG CTG GTT GAC GGA GTG GAG CTT TCA CTG CTG CCG TCT<br>Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser<br>365 370 375 380 | 1200 |
| GAG GGC AAT AAG GCG GCA TTT CAG CAC GAG ATT GAG CAA AAC GGC GTG<br>Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val<br>385 390 395     | 1248 |
| AAG GCA ACG GTG TGT TGT TCC AAC TTG GAT TAC ATG AGT TTT GGG AAG<br>Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys<br>400 405 410     | 1296 |
| CTG TCA AAA GAA AAT AAA GAC GAT ATG TTC CTG CAA GGT GTC CGC ACT<br>Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr<br>415 420 425     | 1344 |
| CCA GTA TCC GAT GTG GCG GCA AGG ACG GAG GCA AAC GCC AAA TAT CGC<br>Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg<br>430 435 440     | 1392 |
| GGT ACT TGG TAC GGA TAT ATT GCC AAC GGC ACA AGC TGG AGC GGC GAA<br>Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu<br>445 450 455 460 | 1440 |
| GCC TCC AAT CAG GAA GGT GGT AAT AGG GCA GAG TTT GAC GTG GAT TTT<br>Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe<br>465 470 475     | 1488 |

TCC ACT AAA AAA ATC AGT GGC ACA CTG ACG GCA AAA GAC CGT ACG TCT 1536  
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser  
 480 485 490  
 CCT GCG TTT ACT ATT ACT GCC ATG ATT AAG GAC AAC GGT TTT TCA GGT 1584  
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly  
 495 500 505  
 GTG GCG AAA ACC GGT GAA AAC GGC TTT GCG CTG GAT CCG CAA AAT ACC 1632  
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr  
 510 515 520  
 GGA AAT TCC CAC TAT ACG CAT ATT GAA GCC ACT GTA TCC GGC GGT TTC 1680  
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe  
 525 530 535 540  
 TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA 1728  
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly  
 545 550 555  
 AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG 1776  
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala  
 560 565 570  
 AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T 1808  
 Lys Arg Gln Gln Leu Val Gln  
 575

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
 -20 -15 -10 -5  
 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
 1 5 10  
 Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu  
 15 20 25  
 Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala  
 30 35 40  
 Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn  
 45 50 55 60  
 Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys  
 65 70 75  
 Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu  
 80 85 90  
 Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp  
 95 100 105

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser  
 110 115 120  
 Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile  
 125 130 135 140  
 Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro  
 145 150 155  
 Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp  
 160 165 170  
 Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser  
 175 180 185  
 Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly  
 190 195 200  
 Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly  
 205 210 215 220  
 Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly  
 225 230 235  
 Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys  
 240 245 250  
 Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn  
 255 260 265  
 Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly  
 270 275 280  
 Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr  
 285 290 295 300  
 Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn  
 305 310 315  
 Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly  
 320 325 330  
 Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg  
 335 340 345  
 Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp  
 350 355 360  
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser  
 365 370 375 380  
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val  
 385 390 395  
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys  
 400 405 410  
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr  
 415 420 425  
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg  
 430 435 440

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu  
 445 450 455 460  
 Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe  
 465 470 475  
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser  
 480 485 490  
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly  
 495 500 505  
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr  
 510 515 520  
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe  
 525 530 535 540  
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly  
 545 550 555  
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala  
 560 565 570

Lys Arg Gln Gln Leu Val Gln  
575

(2) INFORMATION FOR SEQ ID NO: 5:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2255 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: N. meningitidis  
 (B) STRAIN: M978
- 15 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2115
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2115
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGT CTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA 48  
 Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu  
 1 5 10 15  
 GCC CCG CGT CCC GCC CCA AAA TAT CAA GAT GTT TCT TCC GAA AAA CCG 96  
 Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro  
 20 25 30  
 CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA ATG CGC CTC AAG 144  
 Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys  
 35 40 45

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGG CCG AAT TGG CAT CCG CAG GCA AAT CCT AAA GAA GAT GAG ATA AAA | 192 |
| Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys |     |
| 50 55 60                                                        |     |
| CTT TCT GAA AAT GAT TGG GAG GCG ACA GGA TTG CCA GGC AAT CCC AAA | 240 |
| Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys |     |
| 65 70 75 80                                                     |     |
| AAC TTA CCT GAG CGA CAG AAA TCG GTT ATT GAA AAA GTA AAA ACA GGC | 288 |
| Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly |     |
| 85 90 95                                                        |     |
| AGC GAC AGC AAT ATT TAT TCT TCC CCC TAT CTC ACG CAA TCA AAC CAT | 336 |
| Ser Asp Ser Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His     |     |
| 100 105 110                                                     |     |
| CAA AAC GGC AGT GCA AAC CAA CCA AAA AAT GAA GTA AAA GAT TAT AAA | 384 |
| Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys |     |
| 115 120 125                                                     |     |
| GAG TTC AAA TAT GTT TAT TCC GGT TGG TTT TAC AAA CAC GCT AAA CTC | 432 |
| Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu |     |
| 130 135 140                                                     |     |
| GAA ATC ATA AAA GAA AAC AAC TTA ATT AAG GGT GCA AAG AGC GGC GAC | 480 |
| Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp |     |
| 145 150 155 160                                                 |     |
| GAC GGT TAT ATC TTT TAT CAC GGT GAA AAA CCT TCC CGA CAA CTT CCC | 528 |
| Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro |     |
| 165 170 175                                                     |     |
| GTT TCT GGA GAA GTT ACC TAC AAA GGC GTA TGG CAT TTT GTA ACC GAT | 576 |
| Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp |     |
| 180 185 190                                                     |     |
| ACG AAA CAG GGA CAA AAA TTT AAC GAT ATT CTT GGA ACC TCA AAA AAA | 624 |
| Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys |     |
| 195 200 205                                                     |     |
| CAA GGC GAC AGG TAT AGC GGA TTT CCG GGT GAT GAC GGC GAA GAA TAT | 672 |
| Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr |     |
| 210 215 220                                                     |     |
| TCC AAT AAA AAT GAA GCG ACT TTA CAA GGC AGT CAA GAG GGT TAT GGT | 720 |
| Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly |     |
| 225 230 235 240                                                 |     |
| TTT ACC TCA AAT TTA AAA GTG GAT TTC AAT AAG AAA AAA TTG ACG GGT | 768 |
| Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly |     |
| 245 250 255                                                     |     |
| GAA TTG ATA CGC AAT AAT AGA GTT ACA AAC GCT ACT GCT AAC GAT AAA | 816 |
| Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys |     |
| 260 265 270                                                     |     |
| TAC ACC ACC CAA TAT TAC AGC CTT GAG GCT CAA GTA ACA GGC AAC CGC | 864 |
| Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg |     |
| 275 280 285                                                     |     |
| TTC AAC GGC AAG GCA ACG GCA ACC GAC AAA CCT GGC ACT GGA GAA ACC | 912 |
| Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr |     |
| 290 295 300                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAA CAA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC GGC GGC TTT<br>Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe<br>305 310 315 320 | 960  |
| TTC GGC CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG AGC AAC GAT<br>Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp<br>325 330 335     | 1008 |
| CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC CAA GAC AAA GCC GCA<br>Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala<br>340 345 350     | 1056 |
| AAT GGC AAT ACT GCG GCG GCT TCA GGC GGC ACA GAT GCG GCA GCA TCA<br>Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser<br>355 360 365     | 1104 |
| AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG GTT<br>Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val<br>370 375 380     | 1152 |
| TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT CTC<br>Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu<br>385 390 395 400 | 1200 |
| GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG ATT<br>Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile<br>405 410 415     | 1248 |
| CCG CTC CTG CCC GAG ACT TCC GAA AGT GCG AGC AAT CAG GCA GAT AAA<br>Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys<br>420 425 430     | 1296 |
| GGT AAA AAA GGT AAA AAC GGT AAA AAC GGC GGA ACA GAC TTT ACC TAC<br>Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr<br>435 440 445     | 1344 |
| AAA ACA ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC CAA<br>Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln<br>450 455 460     | 1392 |
| ACA GGT GCG GCA GGC TCT AGC GGC GCA CAA ACC GAT TTG GGT AAG GCG<br>Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala<br>465 470 475 480 | 1440 |
| GAC GTT AAC GGC GGT AAG GCA GAA ACA AAA ACC TAT GAA GTC GAA GTC<br>Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val<br>485 490 495     | 1488 |
| TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC GGA ATG TTG ACG CGT AAA<br>Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys<br>500 505 510     | 1536 |
| AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA AAC AGT AGT CAA GCT GAT<br>Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp<br>515 520 525     | 1584 |
| GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG TTC CTC CAA GGC GAG CGT<br>Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg<br>530 535 540     | 1632 |
| ACC GAT GAA AAA GAG ATT CCA AAC GAC CAA AAC GTC GTT TAT CGG GGG<br>Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly<br>545 550 555 560 | 1680 |

TCT TGG TAC GGG CAT ATT GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT 1728  
 Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala  
 565 570 575  
 TCC AAT GCA ACG AGT GGC AAC AGG GCG GAA TTT ACT GTG AAT TTC GAT 1776  
 Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp  
 580 585 590  
 ACG AAA AAA ATT AAC GGC ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA 1824  
 Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala  
 595 600 605  
 ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG 1872  
 Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr  
 610 615 620  
 GCA AAA ACT GCT GAG TTA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC 1920  
 Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr  
 625 630 635 640  
 GGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG CAG GGC GGT TTT 1968  
 Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe  
 645 650 655  
 TAC GGG CCT AAA GCC GAA GAG TTG GCC GGA TGG TTT GCC TAT CCG GGC 2016  
 Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly  
 660 665 670  
 GAT AAA CAA ACG GAA AAG GCA AAG GTT GCA TCC GGC GAT GGA AAT TCA 2064  
 Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser  
 675 680 685  
 GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG 2112  
 Ala Ser Ser Ala Thr Val Phe Gly Ala Lys Arg Gln Gln Pro Val  
 690 695 700  
 CAA TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTGGA TCTTGATTCT 2165  
 Gln  
 705  
 GTGGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTTCTTC CGAAAAACCG 2225  
 CAAGCCCCAA AAGACCAAGG CGGATACGGT 2255

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu  
 1 5 10 15  
 Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro  
 20 25 30  
 Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys  
 35 40 45

Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys  
 50 55 60  
 Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys  
 65 70 75 80  
 Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly  
 85 90 95  
 Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His  
 100 105 110  
 Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys  
 115 120 125  
 Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu  
 130 135 140  
 Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp  
 145 150 155 160  
 Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro  
 165 170 175  
 Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp  
 180 185 190  
 Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys  
 195 200 205  
 Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr  
 210 215 220  
 Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly  
 225 230 235 240  
 Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly  
 245 250 255  
 Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys  
 260 265 270  
 Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg  
 275 280 285  
 Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr  
 290 295 300  
 Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe  
 305 310 315 320  
 Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp  
 325 330 335  
 Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala  
 340 345 350  
 Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser  
 355 360 365  
 Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val  
 370 375 380



Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu  
385 390 395 400  
Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile  
405 410 415  
Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys  
420 425 430  
Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr  
435 440 445  
Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln  
450 455 460  
Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala  
465 470 475 480  
Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val  
485 490 495  
Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys  
500 505 510  
Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp  
515 520 525  
Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg  
530 535 540  
Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly  
545 550 555 560  
Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala  
565 570 575  
Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp  
580 585 590  
Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala  
595 600 605  
Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr  
610 615 620  
Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr  
625 630 635 640  
Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe  
645 650 655  
Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly  
660 665 670  
Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser  
675 680 685  
Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val  
690 695 700  
Gln  
705

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: N. meningitidis  
 (B) STRAIN: 6940
- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2079
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2079
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TGT TTG GGT GGC GGC GGC ACG TTT GAT CTT GAT TCT GTC GAT ACC GAA | 48  |
| Cys Leu Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu     |     |
| 1 5 10 15                                                       |     |
| GCC CCG CGT CCC GAC CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA CCG | 96  |
| Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro |     |
| 20 25 30                                                        |     |
| CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG AAA | 144 |
| Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys |     |
| 35 40 45                                                        |     |
| CGG AGG AAT TGG TAT TCC GCA GCA AAA GAA GAC GAG GTT AAA CTG AAC | 192 |
| Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn |     |
| 50 55 60                                                        |     |
| GAG AGT GAT TGG GAG ACG ACA GGA TTG CCG ACA GAA CCC AAG AAA CTG | 240 |
| Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu |     |
| 65 70 75 80                                                     |     |
| CCA TTA AAA CAA GAA TCC GTC ATT TCA AAA GTA CAA GCA AAC AAT GGC | 288 |
| Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly |     |
| 85 90 95                                                        |     |
| GAC AAC AAT ATT TAC ACT TCC CCC TAT CTC ACG CAA TCA AAC CAT CAA | 336 |
| Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln |     |
| 100 105 110                                                     |     |
| AAT AGC AGC ATT AAT GGC GGT GCA AAC CTG CCA AAA AAC GAA GTA ACA | 384 |
| Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr |     |
| 115 120 125                                                     |     |
| AAT TAT AAA GAT TTC AAA TAT GTT TAT TCC GGC TGG TTT TAT AAA CAT | 432 |
| Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His |     |
| 130 135 140                                                     |     |
| GCT AAA AAC GAA ATC ATA AGA GAA AAC AGC TCA ATT AAG GGT GCA AAG | 480 |
| Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys |     |
| 145 150 155 160                                                 |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC GGC GAC GAC GGC TAT ATC TTT TAT CAC GGC AAA GAA CCT TCC CGA<br>Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg<br>165 170 175     | 528  |
| CAA CTT CCC GCT TCT GGA ACA GTT ACC TAT AAA GGT GTG TGG CAT TTT<br>Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe<br>180 185 190     | 576  |
| GCG ACC GAT GTC AAA AAA TCC CAA AAT TTT CGC GAT ATT ATC CAG CCT<br>Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro<br>195 200 205     | 624  |
| TCG AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCG GGC GAT GAT GAT<br>Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp<br>210 215 220     | 672  |
| GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT CAA GAG<br>Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu<br>225 230 235 240 | 720  |
| GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AGT AAA AAA<br>Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys<br>245 250 255     | 768  |
| TTG ACG GGT AAA TTA ATA CGC AAT AAT AGA GTT ACA AAC GCT CCT ACT<br>Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr<br>260 265 270     | 816  |
| AAC GAT AAA TAC ACC ACC CAA TAC TAC AGC CTT GAT GCC CAA ATA ACA<br>Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr<br>275 280 285     | 864  |
| GGC AAC CGC TTC AAC GGT AAG GCG ATA CGG ACC GAC AAA CCC GAC ACT<br>Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr<br>290 295 300     | 912  |
| GGA GGA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC<br>Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser<br>305 310 315 320 | 960  |
| GGC GGC TTT TTC GGT CCG AAG GGT GAG GAA TTG GGT TTC CGC TTT TTG<br>Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu<br>325 330 335     | 1008 |
| AGC GAC GAT AAA AAA GTT GCG GTT GTC GGC AGC GCG AAA ACC AAA GAC<br>Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp<br>340 345 350     | 1056 |
| AAA ACG GAA AAT GGC GCG GTG GCT TCA GGC GGC ACA GAT GCG GCA GCA<br>Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala<br>355 360 365     | 1104 |
| TCA AAC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG<br>Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr<br>370 375 380     | 1152 |
| GTT TTG GAT GCG GTC GAG CTG AAA TTG GGC GAT AAG GAA GTC CAA AAG<br>Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys<br>385 390 395 400 | 1200 |
| CTC GAC AAC TTC AGC AAC GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG<br>Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met<br>405 410 415     | 1248 |

ATT CCG CTC TTG CCC GAG GCT TCC GAA AGT GGG AAC AAT CAA GCC AAT 1296  
Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn  
420 425 430

CAA GGT ACA AAT GGC GGA ACA GCC TTT ACC CGC AAA TTT GAC CAC ACG 1344  
Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr  
435 440 445

CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG 1392  
Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly  
450 455 460

GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA 1440  
Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
465 470 475 480

ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC 1488  
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
485 490 495

GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA 1536  
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu  
500 505 510

AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG 1584  
Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
515 520 525

TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA 1632  
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln  
530 535 540

AAC ATC GTT TAT CCG GGG TCT TGG TAC GGA TAT ATT GCC AAC GAC AAA 1680  
Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys  
545 550 555 560

AGC ACA AGC TGG AGC GGC AAT GCT TCC AAT GCA ACG AGT GGC AAC AGG 1728  
Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg  
565 570 575

GCG GAA TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACT GGT ACG TTA 1776  
Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu  
580 585 590

ACC GCT GAC AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAT ATT 1824  
Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile  
595 600 605

AAG GAC AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT 1872  
Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe  
610 615 620

GAT CTC GAT CAA AGC AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA 1920  
Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr  
625 630 635 640

GAT GCC AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG 1968  
Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu  
645 650 655

GGC GGA TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG AAA AAT GCA ACA 2016  
Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr  
660 665 670

AAT GCA TCC GGC AAT AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC 2064  
 Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg  
 675 680 685

CAA CAG CCT GTG CGA TAACGCAAGC CCAAAAAGAC CAAGGCGGAT ACGGT 2114  
 Gln Gln Pro Val Arg  
 690

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu  
 1 5 10 15

Ala Pro Arg Pro Asp Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro  
 20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys  
 35 40 45

Arg Arg Asn Trp Tyr Ser Ala Ala Lys Glu Asp Glu Val Lys Leu Asn  
 50 55 60

Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu  
 65 70 75 80

Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly  
 85 90 95

Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln  
 100 105 110

Asn Ser Ser Ile Asn Gly Gly Ala Asn Leu Pro Lys Asn Glu Val Thr  
 115 120 125

Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His  
 130 135 140

Ala Lys Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys  
 145 150 155 160

Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg  
 165 170 175

Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Val Trp His Phe  
 180 185 190

Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro  
 195 200 205

Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp  
 210 215 220

Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly Gln Glu  
 225 230 235 240

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys  
245 250 255  
Leu Thr Gly Lys Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Pro Thr  
260 265 270  
Asn Asp Lys Tyr Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr  
275 280 285  
Gly Asn Arg Phe Asn Gly Lys Ala Ile Arg Thr Asp Lys Pro Asp Thr  
290 295 300  
Gly Gly Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser  
305 310 315 320  
Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu  
325 330 335  
Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp  
340 345 350  
Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp Ala Ala Ala  
355 360 365  
Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr  
370 375 380  
Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys  
385 390 395 400  
Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met  
405 410 415  
Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn  
420 425 430  
Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr  
435 440 445  
Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly  
450 455 460  
Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
465 470 475 480  
Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
485 490 495  
Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu  
500 505 510  
Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
515 520 525  
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln  
530 535 540  
Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys  
545 550 555 560  
Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg  
565 570 575

Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu  
580 585 590

Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile  
595 600 605

Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe  
610 615 620

Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr  
625 630 635 640

Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu  
645 650 655

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr  
660 665 670

Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg  
675 680 685

Gln Gln Pro Val Arg  
690

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
(B) STRAIN: S3032

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..2097

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..2097

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TGT TTG GGC GGA GGC GGC GGC AGT TTC GAT CTT GAT TCT GTC GAT ACC | 48  |
| Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr     |     |
| 1 5 10 15                                                       |     |
| GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT TCC GAA AAA | 96  |
| Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys |     |
| 20 25 30                                                        |     |
| CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG ATG AGG TTG | 144 |
| Pro Gln Ala Gln Lys Asp Gln Gly Tyr Gly Phe Ala Met Arg Leu     |     |
| 35 40 45                                                        |     |
| AAA CGG AGG AAT TGG TAT CCG TCG GCA AAA GAA AAC GAG GTT AAA CTG | 192 |
| Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu |     |
| 50 55 60                                                        |     |

AAT GAG AGT GAT TGG GAG ACG ACA GGA TTG CCA AGC AAT CCC AAA AAC 240  
Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn 80  
65 70 75

TTA CCT GAG CGA CAG AAA TCG GTT ATT GAT CAA GTA GAA ACA GAT GGC 288  
Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly 95  
85 90 95

GAC AGC AAT AAC AGC AAT ATT TAT TCT TCC CCC TAT CTC ACG CAA TCA 336  
Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser 110  
100 105 110

AAC CAT CAA AAC GGC AAC ACT GGC AAC GGT GTA AAC CAA CCA AAA AAC 384  
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn 125  
115 120 125

GAA GTA ACA GAT TAC AAA AAT TTT AAA TAT GTT TAT TCC GGC TGG TTT 432  
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe 140  
130 135 140

TAC AAA CAC GCC AAA CGA GAG GTT AAC TTA GCG GTG GAA CCT AAA ATT 480  
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile 160  
145 150 155 160

GCA AAA AAC GGC GAC GAC GGT TAT ATC TTC TAT CAC GGT AAA GAC CCT 528  
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro 175  
165 170 175

TCC CGA CAA CTT CCC GCT TCT GGA AAA ATT ACC TAT AAA GGT GTG TGG 576  
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp 190  
180 185 190

CAT TTT GCG ACC GAT ACA AAA AGG GGT CAA AAA TTT CGT GAA ATT ATC 624  
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile 205  
195 200 205

CAA CCT TCA AAA AAT CAA GGC GAC AGA TAT AGC GGA TTT TCG GGT GAT 672  
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp 220  
210 215 220

GAT GAT GAA CAA TAT TCT AAT AAA AAC GAA TCC ATG CTG AAA GAT GGT 720  
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly 240  
225 230 235 240

CAT GAA GGT TAT GGT TTT GCC TCG AAT TTA GAA GTG GAT TTC GAC AAT 768  
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn 255  
245 250 255

AAA AAA TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AAC CAA AAT AAT 816  
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn 270  
260 265 270

AAT ACT AAT AAT GAC AAA CAC ACC ACC CAA TAC TAC AGC CTT GAT GCG 864  
Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala 285  
275 280 285

ACG CTT AAG GGA AAC CGC TTC AGC GGA AAA GCG GAA GCA ACC GAC AAA 912  
Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys 300  
290 295 300

CCC AAA AAC GAC GGC GAA ACC AAG GAA CAT CCC TTT GTT TCC GAC TCG 960  
Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser 320  
305 310 315 320



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TCT TCT TTG AGC GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT<br>Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly<br>325 330 335     | 1008 |
| TTC CGC TTT TTG AGC AAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG<br>Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala<br>340 345 350     | 1056 |
| AAA ACC AAA GAC AAA CCC GCA AAT GGC AAT ACT GCG GAG GCT TCA GGC<br>Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly<br>355 360 365     | 1104 |
| GGC ACA GAT GCG GCA GCA TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA<br>Gly Thr Asp Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu<br>370 375 380         | 1152 |
| AAC AGT AAG CTG ACC ACC GTT TTG GAT GCG GTC GAG CTG ACG CAC GGC<br>Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly<br>385 390 395 400 | 1200 |
| GGC ACA GCA ATC AAA AAT CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG<br>Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu<br>405 410 415     | 1248 |
| GTT GTC GAC GGC ATT ATG ATT CCG CTC CTG CCT CAA AAT TCA ACA GGC<br>Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly<br>420 425 430     | 1296 |
| AAA AAT AAT CAG CCC GAT CAA GGT AAA AAC GGC GGA ACA GCC TTT ATC<br>Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile<br>435 440 445     | 1344 |
| TAT AAA ACG ACC TAC ACG CCG AAA AAC GAT GAC AAA GAT ACC AAA GCC<br>Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala<br>450 455 460     | 1392 |
| CAA ACA GTC ACG GGC GGC ACG CAA ACC GCT TCA AAT ACG GCA GGT GAT<br>Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp<br>465 470 475 480 | 1440 |
| GCC AAT GGC AAA ACA AAA ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC<br>Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn<br>485 490 495     | 1488 |
| CTC AAT TAT CTG AAA TAC GGG TTG CTG ACG CGC AAA ACT GCC GGC AAC<br>Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn<br>500 505 510     | 1536 |
| ACG GTG GGA AGC GGC AAC AGC AGC CCA ACC GCC GCC GCC CAA ACG GAC<br>Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp<br>515 520 525     | 1584 |
| GCG CAG AGT ATG TTC CTC CAA GGC GAG CGC ACC GAT GAA AAC AAG ATT<br>Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile<br>530 535 540     | 1632 |
| CCA AGC GAG CAA AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT<br>Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile<br>545 550 555 560 | 1680 |
| GCC AGC AGC ACA AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC<br>Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly<br>565 570 575     | 1728 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC AGG GCG GAA TTT ACT GTG AAT TTT GGC GAG AAA AAA ATT ACC GGC<br>Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly<br>580 585 590     | 1776 |
| ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT<br>Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly<br>595 600 605     | 1824 |
| AAG ATT GAG GGC AAC GGT TTT TCC GGT ACG GCA AAA ACT GCT GAA TTA<br>Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu<br>610 615 620     | 1872 |
| GGT TTT GAT CTC GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT<br>Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr<br>625 630 635 640 | 1920 |
| ATC ACA GAT GCC AAG GTA AAG GGC GGT TTT TAC GGG CCC AAA GCC GAA<br>Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu<br>645 650 655     | 1968 |
| GAG TTG GGC GGA TGG TTT GCC TAT TCG GAC GAT AAA CAA ACG AAA AAT<br>Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn<br>660 665 670     | 2016 |
| GCA ACA GAT GCA TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC<br>Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val<br>675 680 685     | 2064 |
| GTA TTC GGT GCG AAA CGC CAA CAG CCG GTG CAA TAAACCAAGG CCGATAC<br>Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln<br>690 695                              | 2114 |

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Cys | Leu | Gly | Gly | Gly | Gly | Gly | Ser | Phe | Asp | Leu | Asp | Ser | Val | Asp | Thr | 1  | 5  | 10 | 15 |
| Glu | Ala | Pro | Arg | Pro | Ala | Pro | Lys | Tyr | Gln | Asp | Val | Ser | Ser | Glu | Lys | 20 | 25 | 30 |    |
| Pro | Gln | Ala | Gln | Lys | Asp | Gln | Gly | Gly | Tyr | Gly | Phe | Ala | Met | Arg | Leu | 35 | 40 | 45 |    |
| Lys | Arg | Arg | Asn | Trp | Tyr | Pro | Ser | Ala | Lys | Glu | Asn | Glu | Val | Lys | Leu | 50 | 55 | 60 |    |
| Asn | Glu | Ser | Asp | Trp | Glu | Thr | Thr | Gly | Leu | Pro | Ser | Asn | Pro | Lys | Asn | 65 | 70 | 75 | 80 |
| Leu | Pro | Glu | Arg | Gln | Lys | Ser | Val | Ile | Asp | Gln | Val | Glu | Thr | Asp | Gly | 85 | 90 | 95 |    |

Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser  
100 105 110  
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn  
115 120 125  
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe  
130 135 140  
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile  
145 150 155 160  
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro  
165 170 175  
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp  
180 185 190  
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile  
195 200 205  
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp  
210 215 220  
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly  
225 230 235 240  
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn  
245 250 255  
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn  
260 265 270  
Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala  
275 280 285  
Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys  
290 295 300  
Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser  
305 310 315 320  
Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly  
325 330 335  
Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala  
340 345 350  
Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly  
355 360 365  
Gly Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu  
370 375 380  
Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly  
385 390 395 400  
Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu  
405 410 415  
Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly  
420 425 430

Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile  
 435 440 445  
 Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala  
 450 455 460  
 Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp  
 465 470 475 480  
 Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn  
 485 490 495  
 Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn  
 500 505 510  
 Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp  
 515 520 525  
 Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile  
 530 535 540  
 Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile  
 545 550 555 560  
 Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly  
 565 570 575  
 Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly  
 580 585 590  
 Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly  
 595 600 605  
 Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu  
 610 615 620  
 Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr  
 625 630 635 640  
 Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu  
 645 650 655  
 Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn  
 660 665 670  
 Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val  
 675 680 685  
 Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln  
 690 695

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
 (B) STRAIN: IM2169

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly  
 1 5 10 15  
 Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
 35 40 45  
 Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr  
 65 70 75 80  
 Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe  
 85 90 95  
 Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Thr Asp Gln Asn Val Val  
 195

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
 (B) STRAIN: 6940

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
 1 5 10 15  
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
 20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu  
 35 40 45  
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn  
 65 70 75 80  
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Ile Val  
 195

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
 (B) STRAIN: 2223

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
 1 5 10  
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu  
 35 40 45  
 Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn  
 65 70 75 80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Ile Val  
 195

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
 (B) STRAIN: C708

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly  
 1 5 10 15  
 Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
 35 40 45  
 Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn  
 65 70 75 80  
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala  
 100 105 110  
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly  
 115 120 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Asn Asp Gln Asn Val Val  
 195

## (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: N. meningitidis  
 (B) STRAIN: M978

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30  
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp  
 35 40 45  
 Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
 50 55 60  
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly  
 65 70 75 80  
 Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly  
 85 90 95  
 Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp  
 100 105 110  
 Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln  
 115 120 125  
 Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys  
 130 135 140  
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
 145 150 155 160  
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly  
 165 170 175



Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
 180 185 190  
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln  
 195 200 205  
 Asn Val Val  
 210

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*  
 (B) STRAIN: 1610

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Lys Arg Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30  
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly  
 35 40 45  
 Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
 50 55 60  
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly  
 65 70 75 80  
 Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Lys Phe Thr Arg  
 85 90 95  
 Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly  
 100 105 110  
 Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr  
 115 120 125  
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu  
 130 135 140  
 Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr  
 145 150 155 160  
 Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln  
 165 170 175  
 Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu  
 180 185 190  
 Ile Pro Ser Glu Gln Asn Val Val  
 195 200

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: N. meningitidis  
(B) STRAIN: 867

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Thr Lys Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
1 5 10 15  
Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys  
20 25 30  
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
35 40 45  
Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ser  
50 55 60  
Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn  
65 70 75 80  
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
85 90 95  
Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro  
100 105 110  
Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly  
115 120 125  
Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn  
130 135 140  
Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val  
145 150 155 160  
Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly  
165 170 175  
Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile  
180 185 190  
Pro Lys Glu Gln Gln Asp Ile Val  
195 200

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: N. meningitidis  
(B) STRAIN: S3032

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30  
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly  
 35 40 45  
 Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
 50 55 60  
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys  
 65 70 75 80  
 Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr  
 85 90 95  
 Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln  
 100 105 110  
 Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala  
 115 120 125  
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu  
 130 135 140  
 Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr  
 145 150 155 160  
 Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Val Val  
 195

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
 (B) STRAIN: 891

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Thr Lys Asp Lys Pro Gly Asn Gly Ala Arg Leu Gln Ala Ala Arg Cys  
 1 5 10 15

Gly Thr Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys Leu  
                     20                                    25                                    30  
 Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val  
                     35                                    40                                    45  
 Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly  
                     50                                    55                                    60  
 Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Lys Asn Gln  
                     65                                    70                                    75                                    80  
 Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe Glu  
                                     85                                    90                                    95  
 His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly Thr Pro Ser  
                                     100                                    105                                    110  
 Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys  
                                     115                                    120                                    125  
 Thr Lys Thr Tyr Glu Val Asn Leu Cys Ser Asn Leu Asn Tyr Leu Lys  
                                     130                                    135                                    140  
 Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly  
                                     145                                    150                                    155                                    160  
 Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met  
                                     165                                    170                                    175  
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln  
                                     180                                    185                                    190  
 Asn Val Val  
                                     195

## (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT

29

## 10 (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

15

TTTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG 60  
GTGCCTGGGT GCGGGCGGCA GTTTC 85

## (2) INFORMATION FOR SEQ ID NO: 22:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTGTTTTTGT TGAGTGCATG CCTGGGTGGC 30

## 10 (2) INFORMATION FOR SEQ ID NO: 23:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGCGCAAGCT TACAGTTTGT CTTTGTTTTC CGCGCTGCCG 40

## 20 (2) INFORMATION FOR SEQ ID NO: 24:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AAAAAGCATG CATAAAACT ACGCGTTACA CCATTCAAGC 40

## 30 (2) INFORMATION FOR SEQ ID NO: 25:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC 39

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

## (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CGCATCCAAA ACCGTACCTG TGCTGCCTGA

30

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

## (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

## 10 (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GAACATACTT TGTCGTTTT TCGCGTCAA

30

## 20 (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Tyr Lys Gly Thr Trp  
1 5

## 30 (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
(B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

40 Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: N. meningitidis  
(B) STRAIN: IM2394

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 35:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: N. meningitidis  
20 (B) STRAIN: IM2394

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ala Val Phe Gly Ala Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO: 36:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2070 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: BZ83
- (ix) FEATURE:  
35 (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..60
- (ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 61..2067
- 40 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..2067



ATGAACAATCCATTGGTAAATCAGGCTGCTATGGTGGCTGCCTGTGTTTTTGTGAGTGCT 50  
TACTTGTTAGGTAACCATTTAGTCCGACGATACCACGACGGACACAAAAACAATCACGA  
MetAsnAsnProLeuValAsnGlnAlaAlaMetValLeuProValPheLeuLeuSerAla

TGTCTGGGCGGAGGCGGCASITTCGATCTTGAATCTGTGATACCGAAGCCCCGCGTCCC 120  
ACAGACCCGCTCCGCCGTCAAAGCTAGAACTAAGACAGCTATGGCTTCGGGGCGCAGGG  
CysLeuGlyGlyGlyGlySerPheAspLeuAspSerValAspThrGluAlaProArgPro

GCGCCAAAGTATCAAGATGTTCTTCGAAACACCGCAAGCCCCAAAAAGACCAAGGCGGA 180  
CGCGGTTTTCATAGTTCTACAAAGAGGCTTTGTGGCGTTCGGGTTTTTCTGGTTCCGCCT  
AlaProLysTyrGlnAspValSerSerGluThrProGlnAlaGlnLysAspGlnGlyGly

TACGGTTTTTGCAATGCGCTTCAAGCGGCGGAATTGGTACCCAAAAAATGAAGAAGATCAT 240  
ATGCCAAAACGTTACGCGAAGTTCGCCGCTTAACCATGGGTTTTTACTTCTTCTAGTA  
TyrGlyPheAlaMetArgPheLysArgArgAsnTrpTyrProLysAsnGluGluAspHis

AAGGCATTATCAGAAGCGGATTGGGAGAAGTTAGGTGCGGTAAGCCAGATGAGTTTCCC 300  
TTCCGTAATAGTCTTCGCCTAACCTCTTCAATCCACGCCCAATCGGTCTACTCAAAGGG  
LysAlaLeuSerGluAlaAspTrpGluLysLeuGlyAlaGlyLysProAspGluPhePro

CAAAGGAATGAAATATTGAATATGACTGACGGAATTCTGAGTGAGTCTCTTCAGCTGGGT 360  
GTTTCCTTACTTTATAACTTATACTGACTGCCCTTAAGACTCACTCAGAGAAGTCGACCCA  
GlnArgAsnGluIleLeuAsnMetThrAspGlyIleLeuSerGluSerLeuGlnLeuGly

GAGGGCGGGCAAAAGCCGCGTAGAAGGATACACGGATTTCGAATATGTCCGCTCGSGCTAT  
CTCCCGCCGTTTTTCGGCGCATCTTCCTATGTGCCTAAAGGTTATACAGGCGAGCCCGATA  
GluGlyGlyLysSerArgValGluGlyTyrThrAspPheGlnTyrValArgSerGlyTyr  
-----+-----  
ATCTACCGCAACGGTGCCAAATAAATCGATTTCAAAAAAATCGCCCTTTCCGGTCCG  
TAGATGGCGTTGCCACGGTATTTTAGCTAAAGGT.TTTTITTAGCGGGAAAGGCCAGGC  
IleTyrArgAsnGlyAlaAsnLysIleAspPheGlnLysLysIleAlaLeuSerGlyPro  
-----+-----  
GACGGCTACCTTTCTACAAAGGCAGCAATCCTTCCCAAGCTCTGCCGATGGGTAAGGTA  
CTGCCGATGGAAAAGATG.TTCCGTCTTAGGAAGGGTTCGAGACGGCTACCCATTCCAT  
AspGlyTyrLeuPheTyrLysGlySerAsnProSerGlnAlaLeuProMetGlyLysVal  
-----+-----  
GGTTATAAAGGTACTTGGGATTATGTAACCGATGCCAAGATGGGACAAAAATTTCCAG  
CCAATATTTCCATGAACCCTAATACATTGGCTACGGTTCTACCCTGTTTTTAAAGGGTC  
GlyTyrLysGlyThrTrpAspTyrValThrAspAlaLysMetGlyGlnLysPheSerGln  
-----+-----  
TTGGCTGTTTTTCCAGCGGGGGATAGGTATGGGGCTTTGTCTGCCGAGGAAGCGGATGTG  
AACCGACCAAAAGGTCGCCCCCTATCCATACCCGAAACAGACGGCTCCTTCGCCTACAC  
LeuAlaGlyPheProAlaGlyAspArgTyrGlyAlaLeuSerAlaGluGluAlaAspVal  
-----+-----  
TTGCGCAACAAAAGCGAGGCACAGCAAGGTCAGACCGATTTCGGGCTGACCAGCGAGTTT  
AACGCGTTGTTTTCGCTCCGTGTCGTTCAGTCTGGCTAAAGCCCGACTGGTCGCTCAAA  
LeuArgAsnLysSerGluAlaGlnGlnGlyGlnThrAspPheGlyLeuThrSerGluPhe  
-----+-----  
GAGGTGGATTTCGCGGCCAAGACCATGACCGCGCGCTCTACCGCAATAACCGGATTACT  
CTCCACCTAAAGCGGCGGTTCTGGTACTGCGCGCGAGATGGCGTTATTGGCCTAATGA  
GluValAspPheAlaAlaLysThrMetThrGlyAlaLeuTyrArgAsnAsnArgIleThr

ATAACGAAACCGAAATTAAGCCAAACCAATTAAACGTTACGACATTCAGGCTGACCTG 840  
TTATTGCTTTGGCTTTTATTCGGTTTGTTAATTGCAATGCTGTAAGTCCGACTGGAC  
AsnAsnGluThrGluAsnLysAlaLysGlnIleLysArgTyrAspIleGlnAlaAspLeu

CACGGTAACCGCTTCAGCGGCAAGGCAACGGCAACCGACAAACCCAAAAACGACGAAACC 900  
GTGCCATTGGCGAAGTCGCCCTCCGTTGCCGTTGGCTGTTGGGTTATTGCTGCTTTGG  
HisGlyAsnArgPheSerGlyLysAlaThrAlaThrAspLysProLysAsnAspGluThr

AAGGAACATCCCTTTGTTTCCGACTCGTCTTCTTTGAGCGGCGGCTTTTTCGGTCCGAAG 960  
TTCCTTGTAGGAAACAAAGGCTGAGCAGAGAACTCCCGCCGAAAAAGCCAGGCTTC  
LysGluHisProPheValSerAspSerSerSerLeuSerGlyGlyPhePheGlyProLys

GGTGAGGAATTGGGTTTCCGCTTTTGTAGCGACGATCAAAAAGTTGCCGTTGTCCGCAGC 1020  
CCACTCCTTAACCCAAAGGCGAAAACTCGCTGCTAGTTTTTCAACGGCAACAGCCGTCG  
GlyGluGluLeuGlyPheArgPheLeuSerAspAspGlnLysValAlaValValGlySer

GCGAAAACCAAGACAACTGGAAATGGCGCGGCGGCTTCAGGCAGCACAGGTGCCGCA 1080  
CGCTTTTGGTTTCTGTTTGACCTTTTACCGCGCGCGCGAAGTCCGTCGTGTCCACGCCGT  
AlaLysThrLysAspLysLeuGluAsnGlyAlaAlaAlaSerGlySerThrGlyAlaAla

GCATCGGGCGGTGCCGCAGATATGCCGCTCTGAAAACGGTAAGCTGACACGGTTTTGGAT 1140  
CGTAGCCCCGCCACGCCGCTCTATACGGCAGACTTTTGCCATTGCACTGGTGCCAAACCTA  
AlaSerGlyGlyAlaAlaAspMetProSerGluAsnGlyLysLeuThrThrValLeuAsp

GCGGTTGAGCTGAAATCTGGCGGTAAGGAAGTCAAAAATCTCGACAACTTCAGCAATGCC 1200  
CGCCAACTCGACTTTAGACCGCCATTCTTCAGTTTTTAGAGCTGTTGAAGTCGTTACGG  
AlaValGluLeuLysSerGlyGlyLysGluValLysAsnLeuAspAsnPheSerAspAla

-----+-----  
GCCCAACTGTTGTGCGACGGCATTATGATTCCGCTCCTSCCCAGGAATTCCGAAAGCGAG 1260  
-----+-----  
CGGGTTGACCAACAGCTGCCGTAATACTAAGGCGAGGACGGGTTCTTAAGGCTTTCGCTC  
AlaGlnLeuValValAspGlyIleMetIleProLeuLeuProLysAsnSerGluSerGlu  
-----+-----  
AGCAATCAGGCAGATAAAGGTAAAAACGGCGGAACAGCCTTTACCCGCAAATTTGAACAC 1320  
-----+-----  
TCGTTAGTCCGCTCTATTTCCTTTTGGCGCCTTGTCGGAATGGGCGTTTAAACTTGTG  
SerAsnGlnAlaAspLysGlyLysAsnGlyGlyThrAlaPheThrArgLysPheGluHis  
-----+-----  
ACGCCGGAAGTGATAAAAAAGACACCCCAAGCAGGTACGGCGGAGAATGGCAATCCAGCC 1380  
-----+-----  
TGCGGCCTTTCACCTATTTTCTGTGGGTTCTCCATGCCGCTCTTACCGTTAGGTCGG  
ThrProGluSerAspLysLysAspThrGlnAlaGlyThrAlaGluAsnGlyAsnProAla  
-----+-----  
GCTTCAAATACGGCAGGTGATACCAATGGCAAAACAAAAACCTATGAAGTCGAAGTCTGC 1440  
-----+-----  
CGAAGTTTATGCCGTCCTATGGTTACCGTTTGTGTTTTGGATACTTCAGCTTCAGACG  
AlaSerAsnThrAlaGlyAspThrAsnGlyLysThrLysThrTyrGluValGluValCys  
-----+-----  
TGTTCCAACCTCAATTATCTGAAATACGGAATGTTGACGCGTAAAAACAGCAAGTCCGCG 1500  
-----+-----  
ACAAGGTTGGAGTTAATAGACTTTATGCCTTACAACTGCGCATTTTGTCTGTTTCAGGCGC  
CysSerAsnLeuAsnTyrLeuLysTyrGlyMetLeuThrArgLysAsnSerLysSerAla  
-----+-----  
ATGCAGGCAGGCGAAAACGGTAGTCTAGCTGACGCTAAAACGGAACAAGTTGAACAAAGT 1560  
-----+-----  
TACGTCGGTCCGCTTTTGCCATCAGATCGACTGCGATTGCTTGTTCACCTTGTGTTCA  
MetGlnAlaGlyGluAsnGlySerLeuAlaAspAlaLysThrGluGlnValGluGlnSer  
-----+-----  
ATGTTCTCTCAAGGCGAGCGCACCGATGAAAAAGAGATTCCAAAAGAGCAACAAGACATC 1620  
-----+-----  
TACAAGGAGGTTCCGCTCGCGTGGCTACTTTTCTCTAAGGTTTCTCGTTGTTCTGTAG  
MetPheLeuGlnGlyGluArgThrAspGluLysGluIleProLysGluGlnGlnAspIle

GTITATCGGGGGTCTTGGTACGGGCATATTGCCAACGACACAAAGCTGGAGCGGCAATGCT  
-----  
CAAATAGCCCCCAGAACCATGCCCCGATACGGTTGCTGTGTTTCGACCTCGCCGTTACGA 1680  
ValTyrArgGlySerTrpTyrGlyHisIleAlaAsnAspThrSerTrpSerGlyAsnAla

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TCAGATAGAGAGGGCGGCAACAGGGCGGACTTTACCGTGAATTTTGGTACGAAAAAATT  
-----  
AGTCTATCTCTCCGCGCTTGTCCCGCCTGAAATGGCACTTAAAACCATGCTTTTTTTAA 1740  
SerAspArgGluGlyGlyAsnArgAlaAspPheThrValAsnPheGlyThrLysLysIle

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AACGGAACGTTAACCGCTGAAAACAGGCAGGAGGCAACCTTTACCATTGTGGGCGATATT  
-----  
TTGCCTTGCAATTGGCGACTTTGTCCGCTCTCCGTGGAAATGGTAACACCCGCTATAA 1800  
AsnGlyThrLeuThrAlaGluAsnArgGlnGluAlaThrPheThrIleValGlyAspIle

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AAGGACAACGGCTTTGAAGGTACGGCGAAAACCTGCTGACTCAGGTTTGTATCTCGATCAA  
-----  
TTCCTGTTGCCGAAACTTCCATGCCGCTTTTGAAGGACTGAGTCCAAAACCTAGAGCTAGTT 1860  
LysAspAsnGlyPheGluGlyThrAlaLysThrAlaAspSerGlyPheAspLeuAspGln

-----  
AGCAATACCACCCGCACGCCTAAGGCATATATCACAGATGCCAAGGTGAAGGGCGGTTTT  
-----  
TCGTTATGGTGGGCGTGCGGATTCCGTATATAGTGTCTACGGTCCACTTCCCGCCAAAA 1920  
SerAsnThrThrArgThrProLysAlaTyrIleThrAspAlaLysValLysGlyGlyPhe

-----  
TACGGGCCTAAAGCCGAAGAGTTGGGCGGATGTTTGCCTATCCGGGCGATAAACAAACG  
-----  
ATGCCCGGATTTCCGCTTCTCAACCCGCCTACCAAACGGATAGCCCCGCTATTTGTTTGC 1980  
TyrGlyProLysAlaGluGluLeuGlyGlyTrpPheAlaTyrProGlyAspLysGlnThr

GAAAGGCAACGGTTACATCGGGCGATGGAAATTCAGCAAGCAGTGCAACTGTCGTATTC  
 -----  
 CTTTTCGGTGCCAATGTAGGCCGCTACCTTAAAGTCGTTGCTCACGTTGACAGCATAAG  
 -----  
 GluLysAlaThrValThrSerGlyAspGlyAsnSerAlaSerSerAlaThrValValPhe

GGTGC~~GA~~AAACGCCAAAAGCCTGTGCAATAA  
-----  
CCACGCTTTGCGS~~TTT~~TCGACACGTTATT

2070

GlyAlaLysArgGlnLysProValGlnTer

INFORMATION (2) FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 669 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

(2) INFORMATION FOR SEQ ID NO: 38:

- 10            (i)            SEQUENCE CHARACTERISTICS:  
                 (A) LENGTH: 2136 base pairs  
                 (B) TYPE: nucleic acid  
                 (C) STRANDEDNESS: double  
                 (D) TOPOLOGY: linear
- (ii)        MOLECULE TYPE: DNA (genomic)
- 15            (vi)        ORIGINAL SOURCE:  
                 (A) ORGANISM: *Neisseria meningitidis*  
                 (B) STRAIN: BZ163
- (ix)        FEATURE:  
                 (A) NAME/KEY: sig\_peptide  
20                   (B) LOCATION: 1..60
- (ix)        FEATURE:  
                 (A) NAME/KEY: mat\_peptide  
                 (B) LOCATION: 61..2133
- 25            (ix)        FEATURE:  
                 (A) NAME/KEY: CDS  
                 (B) LOCATION: 1..2133

ATGAACAATCCATTGGTAAATCAGGCTGCTATGGTGGTGGCTGTGTTTTGTTGAGTGGCT  
TACTTGTTAGGTAACCATTTAGTCCGACGATACCACGACGGACACAAAAACAACCTCAGCA  
MetAsnAsnProLeuValAsnGlnAlaAlaMetValLeuProValPheLeuLeuSerAla  
TGTTTGGGCGGAGGCGGCATTTGATCTTGATTCTGTGATACCGAAGCCCCCGCTCCC  
ACAAACCCGCTCTCCCTCAAAGCTAGAACTAAGACAGCTATGGCTTCGGGGCGCAGGG  
CysLeuGlyGlyGlyGlySerPheAspLeuAspSerValAspThrGluAlaProArgPro  
GCGCCAAAATATCAAGATGATCTCCGAAAAACCGCAAGCCCAAAAGACCAAGGCGGA  
CGCGGTTTTATAGTTCTACAAGAGAGGCTTTTTGGCGTTCCGGTTTTTCTGGTTCCGCTT  
AlaProLysTyrGlnAspValSerSerGluLysProGlnAlaGlnLysAspGlnGlyGly  
TACGGTTTTGCGATGAGGTTGAAACGGAGGAATCGGCATCCGCAGGCAAAAGAAGACAAA  
ATGCCAAAACGCTACTCCAACCTTTGCTCTTAGCCGTAGGCGTCCGTTTTCTTCTGTTT  
TyrGlyPheAlaMetArgLeuLysArgArgAsnArgHisProGlnAlaLysGluAspLys  
GTTGAACTAAACCCAAATGATTGGGAGGAGACAGGATTGCCGAGCAAGCCCCAAAACCTTA  
CAACTTGATTGGGTTTACTAACCTCTCTGCTCTAACGGCTCGTTCCGGGGTTTTGAAT  
ValGluLeuAsnProAsnAspTrpGluGluThrGlyLeuProSerLysProGlnAsnLeu  
CCCGAGCGACAGCAATCGGTTATTGATAAAGTAAAAACAGACGATGGCAGCAATATTTAC  
GGGCTCGCTGTCGTTAGCCAATAACTATTTTCATTTTGTCTGCTACCGTTCGTTATAAATG  
ProGluArgGlnGlnSerValIleAspLysValLysThrAspAspGlySerAsnIleTyr

ACTTCCCCCTATCTCAGCCAAATCAAACCTCAAAACGGCAGCAGCTAATAGCGGTGCAAAC 420  
TGAAGGGGAATAGAGTGCCTTAGTTTGGTAGTTTGGCCGTCGTGATTATCGCCACGTTTG  
ThrSerProTyrLeuThrGlnSerAsnHisGlnAsnGlySerThrAsnSerGlyAlaAsn  
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CAACCAAAACCAAGTAAAGATTACAAAATTTCAAATATGTTTATTCGGGCTGGTTT 480  
GTTGGTTTTCGCTTCATTTCTAATGTTTAAAGTTTATACAAATAAGGCCGACCAAA  
GlnProLysAsnGluValLysAspTyrLysAsnPheLysTyrValTyrSerGlyTrpPhe  
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TATAAACATGCAGAGAGTGAAGAGAAATTCAGTAAATCAAATTTAAGTCAGGCCGACGAC 540  
ATATTTGTACCTCTCTCACCTCTTAAGTCATTTTAGTTTAAATTCAGTCCGCTGCTG  
TyrLysHisAlaGluSerGluArgGluPheSerLysIleLysPheLysSerGlyAspAsp  
-----  
GGCTATATTTTTTATCACGGTAAAGACCTTCCCGACAACCTCCCACTTCTGAAAAAGTT 600  
CCGATATAAAAAATAGTGCCATTTCTGGGAAGGGCTGTTGAAGGGTGAAGACTTTTTCAA  
GlyTyrIlePheTyrHisGlyLysAspProSerArgGlnLeuProThrSerGluLysVal  
-----  
ATCTACAAAGGCGTATGGCATTITGTAAACCGATACTGAAAAGGGACAAAATTTAACGAT 660  
TAGATGTTTCCGCATACCGTAAACATTGGCTATGACTTTTCCCTGTTTTTAAATTGCTA  
IleTyrLysGlyValTrpHisPheValThrAspThrGluLysGlyGlnLysPheAsnAsp  
-----  
ATTCTTGAAACCTCAAAAGGGCAAGGCGACAGATACAGCGGATTTTCGGGCGATGACGGC 720  
TAAGAACTTTGGAGTTTTCCCGTTCGGCTGTCTATGTCGCCTAAAAGCCCGCTACTGCCG  
IleLeuGluThrSerLysGlyGlnGlyAspArgTyrSerGlyPheSerGlyAspAspGly  
-----  
GAAACAACCTTCCAATAGAACTGATTCCAACCTTAATGATAAGCACGAGGGTTATGGTTTT 780  
CTTTGTTGAAGSTTATCTTGACTAAGGTTTGAATTACTATTTCGTGCTCCCAATACCAAAA  
GluThrThrSerAsnArgThrAspSerAsnLeuAsnAspLysHisGluGlyTyrGlyPhe



ACCTCGAATTAGAAAGTGGATTTGGGCAGTAAAAATTCACGGGTAAATTAATACGCAAT  
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TGGAGCTTAAATCTTCACCTAAAGCGCTCAATTTAACTGCCCATTTAATTATGCGTTA 840  
ThrSerAsnLeuGluValAspPheGlySerLysLysLeuThrGlyLysLeuIleArgAsn

AAATAGAGTTACAAACGCTACTACTAAGCATAAATACACCACCCCAATACTACAGCCTTGAT  
-----  
TTATCTCAATGTTTGGGATGATGATTGCTATTTATGTGTTGGGTTATGATGTCCGAACTA 900  
AsnArgValThrAsnAlaThrThrAsnAspLysTyrThrThrGlnTyrTyrSerLeuAsp

GCCCAAATAACAGGCAACCGCTTCAACGGTAAGGCGATAGCGACCGACAAACCCGACACT  
-----  
CGGGTTTATTGTCCGTTGGCGAAGTGGCCATTCGCTATCGCTGGCTGTTTGGGCTGTGA 960  
AlaGlnIleThrGlyAsnArgPheAsnGlyLysAlaIleAlaThrAspLysProAspThr

GGAGGAACCAAACACTACATCCCTTTGTTCCGACACGTCCTTCTTTGAGCGGCGGCTTTTTTC  
-----  
CCTCCTTGTTTGTATGTAGGGAAACAAAGGCTGAGCGAGAAGAACTCGCCGCCGAAAAAG 1020  
GlyGlyThrLysLeuHisProPheValSerAspSerSerSerLeuSerGlyGlyPhePhe

GGTCCGAAGGGTGAGGAATTGGGTTTCCGCTTTTTGAGCGACGATAAAAAAGTTGCGGTT  
-----  
CCAGGCTTCCCACTCCTTAACCCAAAGCGGAAAAACTCGCTCCTATTTTTCAACGCCAA 1080  
GlyProLysGlyGluGluLeuGlyPheArgPheLeuSerAspAspLysLysValAlaVal

GTCGGCAGCGCGGAAACCAAAGACAAAACGGAAATGGCGCGGTGGCTTCAGGTGGCACA  
-----  
CAGCCGTCGCGCTTTGGTTCTGCTTTGCCTTTACCGCGCCACCGAAGTCCGCGGTGT 1140  
ValGlySerAlaLysThrLysAspLysThrGluAsnGlyAlaValAlaSerGlyGlyThr

GATGCGGCAGCATCAAAACGGTCCGGCAGGCACGTCCTTGGAAAACAGTAAGCTGACCACG  
CTACGCCGTCGTAGTTTCCACGCCGTCCTGCACGACACTTTTGTATTTCGACTGGTGC  
AspAlaAlaAlaSerAsnGlyAlaAlaGlyThrSerSerGluAsnSerLysLeuThrThr

1200

GTTTGGATGCGGTCCAGCTGAAATTGSSCSATAAGGAAGTCCAAAAGCTCGACAACCTTC  
CAAAACCTACGCCAGCTCGACTTAACCCGCTATTCTTCAGGTTTCGAGCTGTTGAAG  
ValLeuAspAlaValGluLeuLysLeuGlyAspLysGluValGlnLysLeuAspAsnPhe

1260

AGCAACGCCGCCCAACTGGTTGTCGACGGCATTATGATTCCGCTCTTGCCCGAGACTTCC  
TCGTTGCGGCGGGTTGACCAACAGCTGCCGTAACTAAAGCGAGAACGGGCTCTGAAGG  
SerAsnAlaAlaGlnLeuValValAspGlyIleMetIleProLeuLeuProGluThrSer

1320

GAAAGTGGGAACAATCAAGCCAATCAAGGTACAAATGGCGGAACAGCCTTTACCCGCAA  
CTTTCACCCCTTGTTAGTTCGGTTAGTTCCATGTTTACCGCCTTGTCGGAAATGGGCGTTT  
GluSerGlyAsnAsnGlnAlaAsnGlnGlyThrAsnGlyGlyThrAlaPheThrArgLys

1380

TTTGACCACACGCCGGAAGTGATAAAAAAGACGCCCAAGCAGGTACGCAGACGAATGGG  
AAACTGGTGTGCGGCCCTTCACTATTTTTCTSCGGGTTTCGTCCATGCGTCTGCTTACCC  
PheAspHisThrProGluSerAspLysLysAspAlaGlnAlaGlyThrGlnThrAsnGly

1440

GCGCAAACCGCTTCAAATACGGCAGGTGATACCAATGGCAAAACAAAAACCTATGAAGTC  
CGCGTTTGGCGAAGTTTATGCCGTCCTACTATGTTACCGTTTGTGTTTGGATACTTCAG  
AlaGlnThrAlaSerAsnThrAlaGlyAspThrAsnGlyLysThrLysThrTyrGluVal

1500

GAAGTCTGCTGTTCCAACTCAATTATCTGAAATACGGAATGTTGACGCGCAAAACAGC  
CTTCAGACGACAAGGTTGAGTTAATAGACTTTATGCCCTTACAACCTSCGCGTTTTTGTGCG  
GluValCysCysSerAsnLeuAsnTyrLeuLysTyrGlyMetLeuThrArgLysAsnSer

1560

AAATCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAGCTGATGCTAAAAACGGAACAAATT  
.....+  
TTCAGGCGCTACGTCCGTCCTCTCTTCGTCATCAGTTCGACTACGATTTTGCCTTGTTCAA  
LysSerAlaMetGlnAlaGlyGluSerSerSerGlnAlaAspAlaLysThrGluGlnVal  
.....+  
1520

GGACAAAGTATGTTCTTCCAAAGGCGAGCGCACCGATGAAAAAGAGATTCCAAGCGAGCAA  
.....+  
CCTGTTTCATACAAAGGAGGTTCCGCTCCGCTGCGTACTTTTCTCTAAGGTTTCGCTCGTT  
GlyGlnSerMetPheLeuGlnGlyGluArgThrAspGluLysGluIleProSerGluGln  
.....+  
1680

AACATCGTTTATCGGGGGTCTTGGTACGGGCATATTGCCAGCAGCACAAAGCTGGAGCGGC  
.....+  
TTGTAGCAAATAGCCCCCAGAAACATGCCCGTATAACGGTCGTCGTGTTTCGACCTCGCCG  
AsnIleValTyrArgGlySerTrpTyrGlyHisIleAlaSerSerThrSerTrpSerGly  
.....+  
1740

AATGCTTCTGATAAAGAGGGCGGCAACAGGGGGGAATTTACTGTGAATTTTGGCGAGAAA  
.....+  
TTACGAAGACTATTTCTCCCGCGTTGTCCCGCTTAAATGACACTTAAAACCGCTCTTT  
AsnAlaSerAspLysGluGlyGlyAsnArgAlaGluPheThrValAsnPheGlyGluLys  
.....+  
1800

AAAATTACCGGCACGTTAACCGCTGAAAACAGGCAGGAGGCAACCTTTACCATTGATGGT  
.....+  
TTTAATGGCCGTGCAATTGGCGACTTTTGTCCGTCCTCCGTTGGAATGGTAACCTACCA  
LysIleThrGlyThrLeuThrAlaGluAsnArgGlnGluAlaThrPheThrIleAspGly  
.....+  
1860

AAGATTGAGGGCAACGGTTTTTCCGGTACGGCAAAACTGCTGAATTAGGTTTGTATCTC  
.....+  
TTCTAACTCCCGTTGCCAAAAAGGCCATGCCGTTTTTGACGACTTAATCCAAACTAGAG  
LysIleGluGlyAsnGlyPheSerGlyThrAlaLysThrAlaGluLeuGlyPheAspLeu  
.....+  
1920

GATCAAAAATAACACCCGACGCTAAGGCATATATCACAGATGCCAAGGTGCAGGGC 1980  
CTAGTTTTTTTATGGTGGGCGTGCGGATTCGGTATATAGTGTCTACGGTTCCACGTCCCG  
AspGlnLysAsnThrThrArgThrProLysAlaTyrIleThrAspAlaLysValGlnGly

GGTTTTTACGGGCCCCAAGCCGAAGAGTTGGGCGGATGGTTTTGCCTATCAGGGCGATAAA 2040  
CCAAAAATGCCCCGGTTTTCGGCTTCTCAACCCGCTACCAAACGGATAGTCCCGCTATTT  
GlyPheTyrGlyProLysAlaGluGluLeuGlyGlyTrpPheAlaTyrGlnGlyAspLys

CAAACGGAAAATACACAGTTCGATCCGCGCAATGGAAATTCAGCAAGCAAGTGCAACTGTC 2100  
GTTTGCCTTTTATGTTGTCAACGTAGGCGCTTACCTTTAAGTCGTTTCGTCACGTTGACAG  
GlnThrGluAsnThrThrValAlaSerGlyAsnGlyAsnSerAlaSerSerAlaThrVal

GTATTCGGTGCAGAAACGCCAAAAGCCTGTGCAATAA 2136  
CATAAGCCACGCTTTGCGGTTTTTCGGACACGTTATT  
ValPheGlyAlaLysArgGlnLysProValGlnTer

## INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 692 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39: